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FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA: 97212 MW: 6FAB16AF85107FE0 CRC64;

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Query Match 83.0%; Score 112; DB 1; Length 856;
 Best Local Similarity 85.7%; Pred. No. 1.5e-08;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Oy 1 RVIRVGRACRAIRHVRIRRGRLRL 28
    ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 RVLEVVGACRAIRHVRIRRGRLRL 855

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RESULT 2
ENV_HV1LM STANDARD: PRT: 856 AA.
AC 070626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=82834;
RX MEDLINE=9517297; PubMed=7826699;
RP SEQUENCE FROM N.A.
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB)."
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC -----
DR EMBL: U12055; AAA76690.1;
DR GYSCOSUDB: 070626;
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW signal.
FT CHAIN 1 30
FT CHAIN 31 511
FT DISULFID 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 216 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA: 96938 MW: 0C241332CFE6687 CRC64;

```

Query Match 83.0%; Score 112; DB 1; Length 856;
 Best Local Similarity 85.7%; Pred. No. 1.5e-08;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

Oy 1 RVIRVGRACRAIRHVRIRRGRLRL 28
    ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 RVLEVVGACRAIRHVRIRRGRLRL 855

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RESULT 3
ENV_HV1BR STANDARD: PRT: 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

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DR EMBL: M12507; AAB12990.1; -
DR HIV: M12507; ENVSMWJ2.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.

FT SIGNAL. 1 29
FT CHAIN 30 501
FT CHAIN 502 847
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 215 244
FT DISULFID 225 236
FT DISULFID 233 326
FT DISULFID 372 435
FT DISULFID 379 408
FT CARBOHYD 87 134
FT CARBOHYD 134 140
FT CARBOHYD 140 151
FT CARBOHYD 151 155
FT CARBOHYD 155 183
FT CARBOHYD 183 184
FT CARBOHYD 184 194
FT CARBOHYD 194 231
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 259 259
FT CARBOHYD 273 273
FT CARBOHYD 286 286
FT CARBOHYD 292 292
FT CARBOHYD 327 327
FT CARBOHYD 334 334
FT CARBOHYD 334 350
FT CARBOHYD 350 356
FT CARBOHYD 356 380
FT CARBOHYD 380 386
FT CARBOHYD 386 390
FT CARBOHYD 390 400
FT CARBOHYD 400 438
FT CARBOHYD 438 450
FT CARBOHYD 450 602
FT CARBOHYD 602 607
FT CARBOHYD 607 616
FT CARBOHYD 616 628
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73AA58CAE CRC64;

Query Match 74.8%; Score 101; DB 1; Length 847;
Best Local Similarity 78.6%; Pred. No. 5; 6e-07;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RYRVQVQACRAIRHIVIRIGRLRL 28
DB 819 RYIEVQVQICRAIRHIVIRIGRLRL 846

RESULT 7
ID ENV_HVIMF STANDARD; PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI:taxid-11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90317877; PubMed-1695254;
RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meler C.,
RA Maslak A.;
RT Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis.";
RJ J. Virol. 64:3792-3803(1990).

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DR EMBL: M33943; AAA44850.1; -
DR HIV: M33943; ENVSMFA.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.

FT SIGNAL. 1 30
FT CHAIN 31 509
FT CHAIN 510 853
FT DISULFID 54 74
FT DISULFID 119 203
FT DISULFID 126 194
FT DISULFID 131 157
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 329
FT DISULFID 376 443
FT DISULFID 383 416
FT DISULFID 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 141 156
FT CARBOHYD 156 160
FT CARBOHYD 160 186
FT CARBOHYD 186 195
FT CARBOHYD 195 232
FT CARBOHYD 232 239
FT CARBOHYD 239 260
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FT CARBOHYD 395 404
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FT CARBOHYD 446 461
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FT CARBOHYD 614 623
FT CARBOHYD 623 635
FT CARBOHYD 635 672
FT CARBOHYD 672 748
FT CARBOHYD 748 748

EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.

FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 3377B993B6F22ABA CRC64;
 Query Match 74.8%; Score 101; DB 1; Length 853;
 Best Local Similarity 82.1%; Pred. No. 5.6e-07;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 RVIRVQACRAIRHIVRIRGRLRL 28
 DB 826 RVIEVQAGAVRAIRHIVRIRGRLRL 853
 RESULT 8
 ENV_HV1B1 STANDARD; PRT; 856 AA.
 ID ENV_HV1B1
 AC P03375;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11678;
 RX MEDLINE=8511123; PubMed=2578615;
 RA Rather L., Haseltine W., Patarca R., Liyak K.J., Starcich B.R., Josephs S.F., Doran E.R., Ratsliski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Pappas T.S., Chirayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;
 RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RT Nature 313:277-284(1985).
 RN (2)
 RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=90285159; PubMed=2355006;
 RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;
 RA "Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells.";
 RT J. Biol. Chem. 265:10373-10382(1990).
 RL J. Biol. Chem. 265:10373-10382(1990).
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 CC -----
 CC EMBL; M15654; AAA44205.1; .
 DR EMBL; M15654; AAA44205.1; .
 DR PIR; A03973; VCLJH3.
 DR HIV; M15654; ENVSRH102.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL.
 FT SIGNAL. 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239

FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
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 FT CARBOHYD 141 141
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 FT CARBOHYD 397 397
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 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
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 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97224 MW; 0BFEB1A18931BB27 CRC64;
 Query Match 74.8%; Score 101; DB 1; Length 856;
 Best Local Similarity 82.1%; Pred. No. 5.6e-07;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 RVIRVQACRAIRHIVRIRGRLRL 28
 DB 828 RVIEVQAGAVRAIRHIVRIRGRLRL 855
 RESULT 9
 ENV_HV1PV STANDARD; PRT; 856 AA.
 ID ENV_HV1PV
 AC P03376;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11700;
 RX MEDLINE=8511157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;
 RA "Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovirus.";
 RT Nature 313:450-458(1985).
 RL Nature 313:450-458(1985).
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[illegible]

FT	CARBOHYD	356	356	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	386	386	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	443	443	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	606	606	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	620	620	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	632	632	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	669	669	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	811	811	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	851 AA;	96644 MW;	D16A3C90857785F1 CRC64;	
OY	1 RVIRVOPACRAIHRIVRIRROGLERIL 28				
	:				
Db	823 RVEIEVGAYRAYRAIRHPRIRROGLELRL 850				
RESULT 12					
ID ENV_HV122	STANDARD;	PRT;	853 AA.		
AC P12487;					
DT 01-OCT-1989 (Rel. 12, Created)					
DT 01-OCT-1989 (Rel. 12, Last sequence update)					
DE 16-OCT-2001 (Rel. 40, Last annotation update)					
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].					
GN ENV.					
OS Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).					
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.					
OX NCBI_TaxID=11683;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Theodore T., Buckler-White A.;					
RL Submitted (NOV-1988) to the HIV data bank.					
CC -----					
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CC -----					
DR EMBL; M22639; AAA45370.1; -.					
DR HIV; M22639; ENV\$Z226.					
DR InterPro; IPR000328; Env_GP41.					
DR InterPro; IPR000777; GP120.					
DR Pfam; PF00516; GP120; 1.					
DR Pfam; PF00517; GP41; 1.					
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.					
KM SIGNAL.					
FT FT 1 31 BY SIMILARITY.					
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.					
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.					
FT DISULFD 53 73 BY SIMILARITY.					
FT DISULFD 118 206 BY SIMILARITY.					
FT DISULFD 125 197 BY SIMILARITY.					
FT DISULFD 130 154 BY SIMILARITY.					
FT DISULFD 219 248 BY SIMILARITY.					
FT DISULFD 229 240 BY SIMILARITY.					
FT DISULFD 297 330 BY SIMILARITY.					
FT DISULFD 376 442 BY SIMILARITY.					
FT DISULFD 383 415 BY SIMILARITY.					
FT CARBOHYD 87 137 N-LINKED (GLCNAC. . .) (POTENTIAL).					
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).					


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FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08CBAFF7008 CRC64;
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Query Match Best Local Similarity 72.6%; Score 98; DB 1; Length 853;
Matches 19; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 RYRVQRACRAIRHVRIRGRLRL 28
|||:|||||:| | |||||:| |
DB 825 RYVEIYRRACRAVLHPRIRGRLRL 852

RESULT 13

ENV_HV1EL STANDARD; PRT; 853 AA.

AC P04581;

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11689;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=86245056; PubMed=2424612;

RT "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";

RL Cell 46:63-74(1986).

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CC EMBL: K03454; AAA44329.1; -

DR EMBL: A07108; CAA00616.1; -

DR HIV: K03454; ENVSELI.

DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
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FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 257 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
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FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAA0D07A5 CRC64;

Query Match Best Local Similarity 71.1%; Score 96; DB 1; Length 853;
Matches 19; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 RYRVQRACRAIRHVRIRGRLRL 28
|||:|||||:| | |||||:| |

DB 825 RYVEIYRRACRAVLHPRIRGRLRL 852

RESULT 14

ENV_HV1A2 STANDARD; PRT; 855 AA.

AC P03378;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11685;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85090453; PubMed=2578227;
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
 RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
 RA Levy J.A., Dina D., Luciw P.A.;
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
 (ARV-2).";
 RL Science. 227:484-492(1985).
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 CC -----
 DR EMBL; K02007; AAB59882.1; -.
 DR PIR; A03976; VCLJ2.
 DR HIV; K02007; ENVSEF2.
 DR InterPro: IPR000328; Env_GPA1.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Aids; Coat protein; Polypotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL. 1 29
 FT CHAIN 30 509
 FT 510 855
 FT DISULFID 53 73
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 FT CARBOHYD 815 815
 FT CARBOHYD 855 AA; 97438 MW; A3BC20573AAC41A2 CRC04;
 SO SEQUENCE

Query Match 69.6%; Score 94; DB 1; Length 855;
 Best local Similarity 75.0%; Pred. No. 5.6e-06;
 Matches 21; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RTIRVQRAIRHVRIRIGLRRL 28
 DB 827 RTIEVAQRAIRAILHRRIRIGLRRL 854
 RESULT 15
 EN_HV1BN STANDARD: PRT: 852 AA.
 ID ENV_HV1BN
 AC P12488;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BR isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89085613; PubMed=2789516;
 RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
 RA Dandekar S.;
 RT "Biological and molecular characterization of human immunodeficiency
 RT virus (HIV-1BR) from the brain of a patient with progressive
 RT dementia.";
 RL Virology 168:79-89(1989).
 CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
 CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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 CC -----
 DR EMBL; M21098; AAA44221.1; -.
 DR PIR; A31667; VCLJBR.
 DR HIV; M21098; ENVSEBVA.
 DR InterPro: IPR000328; Env_GPA1.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Aids; Coat protein; Polypotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL. 1 30
 FT CHAIN 31 507
 FT 508 852
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Query Match 68.1%; Score 92; DB 1; Length 852;

Best Local Similarity 75.0%; Pred. No. 1.1e-05; Mismatches 7; Indels 0; Gaps 0;

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Db 824 RAIEVORAFRAILHPRIRROGLRRIL 851
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Search completed: August 14, 2002, 10:59:44
Job time: 500 sec

